especially prominent within a ~100 kbp region around a centromere where the density effects statistically stretch the chromatin. We also found that a whole region of parameters describing the average state of the chromatin fiber was consistent with the experimental Hi-C data. Finally, the dynamical simulations showed that rapid progression through cell cycle allowed for spatial, but not necessarily topological, equilibration of yeast chromosomes, limiting their mutual entanglement.

2997-Pos Board B152
Interactions of Nuclear Actin-Related Proteins with SWI/SNF Chromatin-Remodeling Complexes
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ATP-dependent chromatin-remodeling complexes (remodelers) modulate chromatin structure and thus play important roles in transcription, DNA replication, and DNA repair. Nuclear actin and actin-related proteins (Arps) are subunits of several such complexes, where they are commonly found in pairs. However, the role of actin/Arps and the mechanism through which they bind the catalytic subunits of their host complexes are unknown. Here, we investigated how budding yeast Arp7 and Arp9 are incorporated into SWI/SNF-family chromatin-remodeling complexes. We present the first biochemical evidence that Arp7 and Arp9 must heterodimerize to bind ATP and interact with the catalytic subunits of the SWI/SNF and RSC complexes. In addition, we present ITC data, which define the remodeler region that interacts with Arp7/9, thus providing a mechanistic framework for understanding how actin/Arps are selectively loaded into their host remodelers.

2998-Pos Board B153
Study of Nuclear Organization through the Dynamic Properties of Chromatin
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Chromosomes occupy specific nuclear volumes called chromosome territories and their motion is highly constrained. Little is known about which proteins and structures organize chromosome territories. A major object of our research is to understand the biophysical mechanisms that maintain this organization. We turned to study the diffusion properties of genome in order to shed light on this maintenance mechanism. The diffusion character of species depends on its properties and on the environment, thereby providing an excellent method for studying the nuclear maintenance mechanism. We examined genome mobility by focusing on three different genomic elements: telomeres, centromeres and specific gene loci. We developed method that allows measuring the diffusion in time-range of 10^{-2} - 10^{4} sec. Such broad time range allowed us to identify the transient anomalous diffusion of different genomic regions that could not be identified by other techniques. Anomalous diffusion usually depends on environmental constrains, such as temporal binding. Therefore, we propose a model for chromatin organization maintenance in the nucleus that is based on temporal binding of chromatin to itself, or to other nuclear entities. In order to prove this hypothesis, we decided to focus on identifying the possible molecular source of the suggested binding. We conduct our research on measuring the effect of loss of Lamin A on chromatin's diffusion properties. We found that telomeres and centromes motion in cells without Lamin A is ~8 times less constrained compared to normal cells. It also shows normal diffusion, while in normal cells diffusion was found anomalous. Based on our results we can conclude that lack of Lamin A leads to looser chromatin. Finding other proteins that are responsible for such binding is a great challenge that we are now pursuing.

2999-Pos Board B154
Exploring the Chromatin Architecture in Living Cells by Minutes-Long Tracking of Gold Nanoparticles
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Investigating the chromatin compaction on the micro(nano)-meter scale, has become a question of interest to understand many cellular processes. Previous evidence suggests that the cell nucleus is spatially heterogeneous and with inaccessible regions mainly due to a high concentration of chromatin. However, the in vivo 3D picture of the nuclear structure remains unclear. In this work, we studied chromatin organization applying the orbital 3D tracking technique to 20 nm gold nanoparticles (NPs) previously incorporated inside the nucleus of NIH3T3 live cells. We have recently shown that metallic NPs do not bleach or blink upon continuous illumination, are extremely stable, very bright and their luminescence spans over the visible spectrum. These characteristics allow us to track them for minutes thus providing 3D trajectories appreciably longer than those based on fluorescent proteins or quantum dots. For this study we have analyzed the motion of 60 NPs. Each one provided us with a ~5 - 30 minutes long trajectory. In ~30% of the cases, we have observed that the NPs remain in regions of apparent confined motion (clusters) and eventually they undergo a long (in the micrometer range) excursion. We have found that the NPs always move faster within the clusters but slower while travelling between two clusters. These results suggest that the NPs get trapped into cavities where they can move relatively fast and eventually get transported (as seen by MSD analysis) from one cavity to the next one along segments of slower diffusion. Additionally, in all the cases analyzed, the NPs showed an increased intensity while moving between two cavities.
This work was supported by the National Center for Research Resources (NCRR, 5P41RR003155) the National Institute of General Medical Sciences (NIGMS, 8P41GM103540) and the University of California, Irvine.

3000-Pos Board B155
Distinct Dosage Compensation Effects by Subunits of Drosophila MSL Complexes
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Epigenetic regulation at the chromosomal level compensates for the difference in the dosage of X-linked genes between the sexes (dosage compensation). In Drosophila, this regulatory mechanism operates through the MSL complex that enhances the transcription of many genes on the X chromosome in males. The results of an investigation of the structural effects of various subunits of the complex confirmed that enriched, specific acetylation of histone H4 at lysine 16 by the histone acetyl transferase subunit MOF induced a more disorganized state of reconstituted single chromatin fibers. In addition, targeting of the MSL complex to plasmids by inclusion of the MSL assembly locus reduced the level of negative supercoiling. Similar targeting of incomplete complexes distinguished the roles that the various subunits of the complex play in this topological modification. Finally, the potential contribution of ISWI containing remodeling complexes to the architecture of compensated chromatin was analyzed and the results indicate a probable role for this remodeling factor in dosage compensation.

3001-Pos Board B156
Rabl Organization of Chromosomes in the Yeast Nucleus
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The location of genes in the interphase nucleus can influence gene expression and recombination. We examine a random walk polymer model of an interphase yeast chromosome that takes into account Rabl organization, namely attachment of the centromere to the spindle pole body, and tethering of the telomeres to the nuclear membrane. using this model, we calculate the probability distribution for the spatial positioning of a single genetic locus on chromosome III and compare it to an experimental distribution obtained by fluorescence microscopy of wild-type yeast cells. To best fit the model to the experimental distribution, the parameters for chromatin rigidity and nuclear architecture are optimized using values within the ranges reported by previous studies. We then quantitatively test the model using a yeast mutant in which the telomeres are not tethered to the nuclear envelope. The mutant's experimental and computational distributions quantitatively agree, which is evidence that a random walk polymer model of yeast chromosomes that incorporates Rabl organization can account for the spatial positioning of genetic loci during interphase. Further studies will apply this model to the understanding of homologous recombination, specifically in the context of double strand break repair.

3002-Pos Board B157
Single-Molecule Studies of a ParB Family Chromosome Segregation Protein from *Bacillussubtilis*
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ParAB systems play a role in chromosome segregation in a wide range of bacterial species. The DNA binding protein ParB (termed Spo0J in *Bacillus*